CLAIMS

What is claimed is:

1. An isolated polynucleotide comprising a nucleotide sequence encoding a first polypeptide of at least 50 amino acids that has at least 60% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NOs:4, 6, 8, 10, 14, 20 and 22,

or an isolated polynucleotide comprising the complement of the nucleotide sequence.

2. An isolated polynucleotide comprising a nucleotide sequence encoding a first polypeptide of at least 50 amino acids that has at least 85% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NOs:18 and 20.

3. An isolated polynucleotide comprising a nucleotide sequence encoding a first polypeptide of at least 50 amino acids that has at least 80% identity based on the Clustal method of alignment when compared to a polypeptide of SEQ ID NO:2.

4. The isolated polynucleotide of Claim 1, wherein the isolated nucleotide sequence consists of a nucleic acid sequence selected from the group consisting of SEQ ID NOs:1, 7, 13, 15, and 21 that codes for the polypeptide selected from the group consisting of SEQ ID NOs:2, 8, 14, 16, and 22.

5. The isolated polynucleotide of Claim 1 wherein the isolated polynucleotide is DNA.

6. The isolated polynucleotide of Claim 1 wherein the isolated polynucleotide is RNA.

7. A chimeric gene comprising the isolated polynucleotide of Claim 1 operably linked to suitable regulatory sequences.

8. An isolated host cell comprising the chimeric gene of Claim 7.

9. An isolated host cell comprising an isolated polynucleotide of Claim 1.

10. The isolated host cell of Claim 7 wherein the isolated host selected from the group consisting of yeast, bacteria, plant, and virus.

11. A virus comprising the isolated polynucleotide of Claim 1.

12. A polypeptide of at least 50 amino acids that has at least 60% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of a diacylglycerol acyltransferase polypeptide of SEQ ID NOs:4, 6, 8, 10, 14, 20 and 22.

13. A polypeptide of at least 50 amino acids that has at least 85% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NOs:18 and 20.

14. A polypeptide of at least 50 amino acids that has at least 80% identity based on the Clustal method of alignment when compared to a polypeptide of SEQ ID NO:2.

15. A method of selecting an isolated polynucleotide that affects the level of expression of a diacylglycerol acyltransferase polypeptide in a plant cell, the method comprising the steps of:

(a) constructing an isolated polynucleotide comprising a nucleotide sequence of at least one of 30 contiguous nucleotides derived from a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1, 3, 5, 7, 11, 13, 15, 17, 19, 21, and the complement of such nucleotide sequences;

(b) introducing the isolated polynucleotide into a plant cell;

(c) measuring the level of a polypeptide in the plant cell containing the polynucleotide; and

(d) comparing the level of polypeptide in the plant cell containing the isolated polynucleotide with the level of polypeptide in a plant cell that does not contain the isolated polynucleotide.

16. The method of Claim 15 wherein the isolated polynucleotide consists of a nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 3, 5, 7, 11, 13, 15, 17, 19 and 21 that codes for the polypeptide selected from the group consisting of SEQ ID NOs:2, 4, 6, 8, 10, 12, 14, 16, 18, 20 and 22.

17. A method of selecting an isolated polynucleotide that affects the level of expression of a diacylglycerol acyltransferase polypeptide in a plant cell, the method comprising the steps of:

(a) constructing an isolated polynucleotide of Claim 1;

(b) introducing the isolated polynucleotide into a plant cell; and

(c) measuring the level of diacylglycerol acyltransferase polypeptide in the plant cell containing the polynucleotide.

18. A method of obtaining a nucleic acid fragment encoding a diacylglycerol acyltransferase polypeptide comprising the steps of:

(a) synthesizing an oligonucleotide primer comprising a nucleotide sequence of at least one of 30 contiguous nucleotides derived from a nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, and the complement of such nucleotide sequences; and

(b) amplifying a nucleic acid sequence using the oligonucleotide primer.

19. A method of obtaining a nucleic acid fragment encoding the amino acid sequence encoding a diacylglycerol acyltransferase polypeptide comprising the steps of:

(a) probing a cDNA or genomic library with an isolated polynucleotide comprising a nucleotide sequence of at least one of 30 contiguous nucleotides derived from

a nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, and the complement of such nucleotide sequences;

(b) identifying a DNA clone that hybridizes with the isolated polynucleotide;

(c) isolating the identified DNA clone; and

(d) sequencing the cDNA or genomic fragment that comprises the isolated DNA clone.

20. A method for evaluating at least one compound for its ability to inhibit the activity of a diacylglycerol acyltransferase, the method comprising the steps of:

(a) transforming a host cell with a chimeric gene comprising a nucleic acid fragment encoding a diacylglycerol acyltransferase, operably linked to suitable regulatory sequences;

(b) growing the transformed host cell under conditions that are suitable for expression of the chimeric gene wherein expression of the chimeric gene results in production of the diacylglycerol acyltransferase encoded by the operably linked nucleic acid fragment in the transformed host cell;

(c) optionally purifying the diacylglycerol acyltransferase expressed by the transformed host cell;

(d) treating the diacylglycerol acyltransferase with a compound to be tested; and

(e) comparing the activity of the diacylglycerol acyltransferase that has been treated with a test compound to the activity of an untreated diacylglycerol acyltransferase, thereby selecting compounds with potential for inhibitory activity.

21. A composition comprising the isolated polynucleotide of Claim 1, Claim 2 or Claim 3.

22. A composition comprising the polypeptide of Claim 12, Claim 13 or Claim 14.

23. An isolated polynucleotide of Claim 1 comprising the nucleotide sequence comprising at least one of 30 contiguous nucleotides of a nucleic sequence selected from the group consisting of SEQ ID NOs:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, and the complement of such sequences.

24. An expression cassette comprising an isolated polynucleotide of Claim 1, Claim 2 or Claim 3 operably linked to a promoter.

25. A method for positive selection of a transformed cell comprising:

(a) transforming a plant cell with an expressiosn cassette of Claim 24; and

(b) growing the transformed plant cell under conditions allowing expression of the polynucleotide in an amount sufficient to modify oil content in the plant cell to provide a positive selection means.